

RAW SEQUENCE LISTING

DATE: 12/11/2001

PATENT APPLICATION: US/10/001,863

TIME: 12:10:36

Input Set : A:\isph-618sequence.txt

Output Set: N:\CRF3\12112001\I001863.raw

ENTERED

5 <110> APPLICANT: James Karras
6 Erich Koller
8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF TOLL-LIKE RECEPTOR 4 EXPRESSION
10 <130> FILE REFERENCE: ISPH-0618
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/001,863
C--> 12 <141> CURRENT FILING DATE: 2001-11-19
12 <160> NUMBER OF SEQ ID NOS: 33
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Antisense Oligonucleotide
24 <400> SEQUENCE: 1
25 tccgtcatcg ctcctcaggg 20
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 20
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense Oligonucleotide
35 <400> SEQUENCE: 2
36 atgcattctg cccccaagga 20
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 3811
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <220> FEATURE:
45 <221> NAME/KEY: CDS
46 <222> LOCATION: (285)...(2684)
48 <400> SEQUENCE: 3
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50 gcctggcttg gactctgac ccagccatgg ccttctctc ctgcgtgaga ccagaaagct 120
51 gggagccctg cgtggagact tggccctaaa ccacacagaa gagctggcat gaaaccaga 180
52 gctttcagac tccggagcct cagcccttca ccccgattcc attgcttctt gctaaatgct 240
53 gccgttttat cacggagggtg gttcctaata ttacttatca atgc atg gag ctg aat 296
54 Met Glu Leu Asn
55 1
57 ttc tac aaa atc ccc gac aac ctc ccc ttc tca acc aag aac ctg gac 344
58 Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp
59 5 10 15 20
61 ctg agc ttt aat ccc ctg agg cat tta ggc agc tat agc ttc ttc agt 392
62 Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser
63 25 30 35
65 ttc cca gaa ctg cag gtg ctg gat tta tcc agg tgt gaa atc cag aca 440
66 Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr

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67	40	45	50	
69 att gaa gat ggg gca tat cag agc cta agc cac ctc tct acc tta ata	488			
70 Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile				
71	55	60	65	
73 ttg aca gga aac ccc atc cag agt tta gcc ctg gga gcc ttt tct gga	536			
74 Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly				
75	70	75	80	
77 cta tca agt tta cag aag ctg gtg gct gtg gag aca aat cta gca tct	584			
78 Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser				
79	85	90	95	100
81 cta gag aac ttc ccc att gga cat ctc aaa act ttg aaa gaa ctt aat	632			
82 Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn				
83	105	110	115	
85 gtg gct cac aat ctt atc caa tct ttc aaa tta cct gag tat ttt tct	680			
86 Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser				
87	120	125	130	
89 aat ctg acc aat cta gag cac ttg gac ctt tcc agc aac aag att caa	728			
90 Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln				
91	135	140	145	
93 agt att tat tgc aca gac ttg cgg gtt cta cat caa atg ccc cta ctc	776			
94 Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln Met Pro Leu Leu				
95	150	155	160	
97 aat ctc tct tta gac ctg tcc ctg aac cct atg aac ttt atc caa cca	824			
98 Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn Phe Ile Gln Pro				
99	165	170	175	180
101 ggt gca ttt aaa gaa att agg ctt cat aag ctg act tta aga aat aat	872			
102 Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn				
103	185	190	195	
105 ttt gat agt tta aat gta atg aaa act tgt att caa ggt ctg gct ggt	920			
106 Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly				
107	200	205	210	
109 tta gaa gtc cat cgt ttg gtt ctg gga gaa ttt aga aat gaa gga aac	968			
110 Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Gly Asn				
111	215	220	225	
113 ttg gaa aag ttt gac aaa tct gct cta gag ggc ctg tgc aat ttg acc	1016			
114 Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr				
115	230	235	240	
117 att gaa gaa ttc cga tta gca tac tta gac tac tac ctc gat gat att	1064			
118 Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile				
119	245	250	255	260
121 att gac tta ttt aat tgt ttg aca aat gtt tct tca ttt tcc ctg gtg	1112			
122 Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser Phe Ser Leu Val				
123	265	270	275	
125 agt gtg act att gaa agg gta aaa gac ttt tct tat aat ttc gga tgg	1160			
126 Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp				
127	280	285	290	
129 caa cat tta gaa tta gtt aac tgt aaa ttt gga cag ttt ccc aca ttg	1208			
130 Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu				
131	295	300	305	

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133 aaa ctc aaa tct ctc aaa agg ctt act ttc act tcc aac aaa ggt ggg 1256
134 Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly
135      310      315      320
137 aat gct ttt tca gaa gtt gat cta cca agc ctt gag ttt cta gat ctc 1304
138 Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu
139 325      330      335      340
141 agt aga aat ggc ttg agt ttc aaa ggt tgc tgt tct caa agt gat ttt 1352
142 Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe
143      345      350      355
145 ggg aca acc agc cta aag tat tta gat ctg agc ttc aat ggt gtt att 1400
146 Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile
147      360      365      370
149 acc atg agt tca aac ttc ttg ggc tta gaa caa cta gaa cat ctg gat 1448
150 Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp
151      375      380      385
153 ttc cag cat tcc aat ttg aaa caa atg agt gag ttt tca gta ttc cta 1496
154 Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu
155      390      395      400
157 tca ctc aga aac ctc att tac ctt gac att tct cat act cac acc aga 1544
158 Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg
159 405      410      415      420
161 gtt gct ttc aat ggc atc ttc aat ggc ttg tcc agt ctc gaa gtc ttg 1592
162 Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu Glu Val Leu
163      425      430      435
165 aaa atg gct ggc aat tct ttc cag gaa aac ttc ctt cca gat atc ttc 1640
166 Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe
167      440      445      450
169 aca gag ctg aga aac ttg acc ttc ctg gac ctc tct cag tgt caa ctg 1688
170 Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu
171      455      460      465
173 gag cag ttg tct cca aca gca ttt aac tca ctc tcc agt ctt cag gta 1736
174 Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val
175      470      475      480
177 cta aat atg agc cac aac aac ttc ttt tca ttg gat acg ttt cct tat 1784
178 Leu Asn Met Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr
179 485      490      495      500
181 aag tgt ctg aac tcc ctc cag gtt ctt gat tac agt ctc aat cac ata 1832
182 Lys Cys Leu Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile
183      505      510      515
185 atg act tcc aaa aaa cag gaa cta cag cat ttt cca agt agt cta gct 1880
186 Met Thr Ser Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala
187      520      525      530
189 ttc tta aat ctt act cag aat gac ttt gct tgt act tgt gaa cac cag 1928
190 Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln
191      535      540      545
193 agt ttc ctg caa tgg atc aag gac cag agg cag ctc ttg gtg gaa gtt 1976
194 Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val
195      550      555      560
197 gaa cga atg gaa tgt gca aca cct tca gat aag cag ggc atg cct gtg 2024

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198 Glu Arg Met Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val
199 565                               570                               575                               580
201 ctg agt ttg aat atc acc tgt cag atg aat aag acc atc att ggt gtg 2072
202 Leu Ser Leu Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val
203                               585                               590                               595
205 tcg gtc ctc agt gtg ctt gta gta tct gtt gta gca gtt ctg gtc tat 2120
206 Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr
207                               600                               605                               610
209 aag ttc tat ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt 2168
210 Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly
211                               615                               620                               625
213 aga ggt gaa aac atc tat gat gcc ttt gtt atc tac tca agc cag gat 2216
214 Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp
215                               630                               635                               640
217 gag gac tgg gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg 2264
218 Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val
219 645                               650                               655                               660
221 cct cca ttt cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg 2312
222 Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val
223                               665                               670                               675
225 gcc att gct gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag 2360
226 Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys
227                               680                               685                               690
229 gtg att gtt gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc 2408
230 Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile
231                               695                               700                               705
233 ttt gaa tat gag att gct cag acc tgg cag ttt ctg agc agt cgt gct 2456
234 Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala
235                               710                               715                               720
237 ggt atc atc ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg 2504
238 Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg
239 725                               730                               735                               740
241 cag cag gtg gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag 2552
242 Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu
243                               745                               750                               755
245 tgg gag gac agt gtc ctg ggg cgg cac atc ttc tgg aga cga ctc aga 2600
246 Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg
247                               760                               765                               770
249 aaa gcc ctg ctg gat ggt aaa tca tgg aat cca gaa gga aca gtg ggt 2648
250 Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly
251                               775                               780                               785
253 aca gga tgc aat tgg cag gaa gca aca tct atc tga agaggaaaaa 2694
254 Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile
255                               790                               795
257 taaaaacctc ctgaggcatt tcttgcccag ctgggtccaa cacttggttca gttaataagt 2754
258 attaaatgct gccacatgtc aggccttatg ctaagggtga gtaattccat ggtgcactag 2814
259 atatgcaggg ctgctaattc caaggagctt ccagtgcaga gggaataaat gctagactaa 2874
260 aatacagagt cttccagggt ggcatittcaa ccaactcagt caaggaaccc atgacaaaga 2934
261 aagtcatttc aactcttacc tcatcaagtt gaataaagac agagaaaaca gaaagagaca 2994

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262 ttgttctttt cctgagtctt ttgaatggaa attgtattat gttatagcca tcataaaacc 3054
263 attttggttag ttttgactga actgggtgtt cactttttcc tttttgattg aatacaattt 3114
264 aaattctact tgatgactgc agtcgtcaag gggctcctga tgcaagatgc cccttccatt 3174
265 ttaagtctgt ctccttacag aggttaaagt ctaatggcta attcctaagg aaacctgatt 3234
266 aacacatgct cacaaccatc ctggtcattc tcgaacatgt tctatttttt aactaatcac 3294
267 ccctgatata tttttatttt tatatatcca gttttcattt ttttacgtct tgcctataag 3354
268 ctaatatcat aaataaggtt gtttaagacy tgcttcaa atccatatta accactattt 3414
269 ttcaagggaag tatggaaaag tacactctgt cactttgtca ctcgatgtca ttccaaagtt 3474
270 attgcctact aagtaatgac tgtcatgaaa gcagcattga aataatttgt ttaaaggggg 3534
271 cactctttta aacgggaaga aaatttccgc ttctgtgtct tatcatggac aatttgggct 3594
272 ataggcatga aggaagtggg attacctcag gaagtcacct tttcttgatt ccagaaacat 3654
273 atgggctgat aaacccgggg tgacctcatg aaatgagttg cagcagatgt ttattttttt 3714
274 cagaacaagt gatgtttgat ggacctatga atctatttag ggagacacag atggctggga 3774
275 tccctcccct gtaaccttct cactgacagg agaacta 3811
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278 <211> LENGTH: 20
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
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283 <223> OTHER INFORMATION: Antisense Oligonucleotide
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286 agagtcccag ccaggcgcga 20
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289 <211> LENGTH: 20
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291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
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296 <400> SEQUENCE: 5
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299 <210> SEQ ID NO: 6
300 <211> LENGTH: 20
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
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311 <211> LENGTH: 20
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321 <210> SEQ ID NO: 8
322 <211> LENGTH: 20
323 <212> TYPE: DNA

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date